

FEATURES source	DEFINITION
Location/Qualifiers	TCBAP1D2669 Pediatric pre-B cell acute lymphoblastic leukemia
1..1078	Baylor-HGSC project-TCB1 Homo sapiens cDNA clone TCBP2669, mRNA
/organism="Homo sapiens"	sequence.
/mol_type="mRNA"	/bases 1 to 508)
/db_xref="taxon:9606"	1
/clone="IM48:5202008"	Wei, Y., Tsang, Y.T.M., Mei, G., Kui, J.M., Ali-Osman Jr., P.R., Muzny, D.
/tissue="Type:1"lymphoma, cell line"	Bouck, J., Gibbs, R.A. and Margolin, J.P.
/lab_host="DH110B (phage-resistant)"	Pediatric Leukemia cDNA sequencing Project.
/clone lib="NIH MGC 99"	Unpublished
/note="organ: lymph, vector: pmp1, site_1: XbaI, site_2: EcoRI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adapter: GGCACGAGG). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and SuperScript II RT (Life Technologies). Note: this is a NIH_MGC Library."	Contact: Dr. Judith P. Margolin Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA
BASE COUNT	108
ORIGIN	1 others
Query Match	40.7%; Score 508.8; DB 12; Length 1078;
Best Local Similarity	96.1%; Pred. No. 4, 6e-126; Mismatches 23; Indels 2; Gaps 1;
Matches	243 a 306 c 309.9 219 t
QY	16 CCGAGGCTGGCCCTGCTCTGCGCCCTGAGGGCGCTCGAG-GGAGGCC
Db	108 CCCAGACAGACCTGAGCTCTGGCGCCCTCCCGAGAGAAGAGAGGCC
QY	74 GCTGGCCCTCCCGAAATGAGCGCTCTCCAGACTCAGCGTACTGACT
Db	168 GTCGGCCCTCCCGAAATGAGCTCTGGCGCCCTCCCGAGAGAAGAGGCC
QY	134 GGTCCCTGGGTTGGACACCCCGAGATGAGCTTGTGAGTTGTGCGCT
Db	228 GGTCTCCAGGCTTGGACACCCCGAGATGAGCTTGTGCGCT
QY	194 CCACCGTAGAGCTGGCGGAAGTGAGAGTGCGGAGCAGGGCTGCT
Db	288 CCACCTCTAGAGGGTGGCGGAAGTGAGAGTGCGGAGCAGGGCTGCT
QY	254 CTATGAGTGCTGAAAGAACAGGACCTACAGAACAGTCAAGGACCG
Db	348 CTATGAGTGCTGAAAGAACAGTCAAGAACAGTCAAGGACCG
QY	314 TTCTCCAGCTCAAGTCCCGTGGAGTCGATACCTGGATTCCTTGGAG
Db	408 TTCTCCAGCTCAAGTCCCGTGGAGTCGATACCTGGATTCCTTGGAG
QY	374 TGGCCCGCCACCTGCTGGCTTACCCAGAGGGAGTCTGAGTCCATG
Db	468 TGGCCCGCCACCTGCTGGCTTACCCAGAGGGAGTCTGAGTCCATG
QY	434 CCAGTACAGCTGGCCCGCTGAGTGAATGAGTGGCGTCACT
Db	528 CCAGTACAGCTGGCCCGCTGAGTGAATGAGTGGCGTCACT
QY	494 GGAGGG
Db	588 GGAGGG
QY	554 AGATCACTCTGGCCGGCTGGCCGGAGACCACTCTGGCCGGAGCTTC
Db	648 AGATCACTCTGGCCGGAGACCACTCTGGCCGGAGCTTC
QY	614 CGTTCAGTGTCCGGAAATACAGCAAGTCTAGGCCACCTGCTCT
Db	708 CGTTCAGTGTCCGGAAATACAGCAAGTCTAGGCCACCTGCTCT
RESULT 2	BB244935
LOCUS	BB244935
508 bp	mRNA
linear	EST 03-OCT-2001
FAX: 832-824-4536	
TEL: 832-824-4536	
EMAIL: clonese@txcc.org	
Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)	
Seq primer: M13 primer.	
FEATURES source	Location/Qualifiers
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/mol_type="mRNA"	/bases 1 to 508)
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/tissue_type="leukopheresis"	Bouck, J., Gibbs, R.A. and Margolin, J.P.
/cell_type="pre-B cell"	Pediatric Leukemia cDNA sequencing Project.
/dev_stage="pediatric 2 years"	Unpublished
/lab_host="DH110B"	Contact: Dr. Judith P. Margolin Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA
QY	/note="vector: lambda psi, Site_1: BamHI, Site_2: EcoRI, First strand cDNA was primed with an anchored XbaI-oligo(dT) primer (5'-GGAGCTCTGAGCGGAGGAGG(T)VN
Db	3; V= A, C, G, N=A, C, T) and then dG tailed. Second strand was primed with a BamHI-3C primer: 5'-AGAGAGCTCGATCGCGCCGCGATATATAT(C) 3').
QY	Double-stranded cDNA was then digested with BamHI and xbaI and directionally cloned into the BamHI and Sall sites of lambda PSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci, P., Weatover, A., Nishiyama, Y., Ohsumi, T., Itoh, M., Nagao, S., Sasaki, N., Okazaki, Y., Muraatsu, M., Schneider, C., Hayashizaki, Y., High efficiency selection of full-length cDNA by improved biotinylated cap trapper, DNA Res 4, 1, 61-6, Pub 28, 1997)"
BASE COUNT	108
ORIGIN	147 a 160 c 93 t
Query Match	32.4%; Score 477.6; DB 10; Length 508;
Best Local Similarity	98.4%; Pred. No. 1, 6e-98; Mismatches 4; Indels 4; Gaps 2;
Matches	504
QY	79 TCAGGCCACCCACAGAGCTGGAGAGGGGGCTCTGGAGGGAGG
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QY	88 AGGAGATGAGGGAGAGAGAGCTGGCTGAGCTCCAGGCTACATT
Db	61 AGGAGATGAGGGAGAGAGAGCTGGCTGAGCTCCAGGCTACATT
QY	918 CTTCTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
Db	120 CTTCTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
QY	978 CAGGAGGCCAGGGCTCTGGAGGAGGAGGAGGAGGAGGAGGAGG

Db	177	CAGGGAGSCCCAGGGCTCTCTGGTCCAGGAAAGGAGCTGCTGTTGGGTTCTAG	236
Qy	1 038	ACAGAGGAGGAGGAGGACTTGATGAGTCTCTCTGGAGAAGGGTTGGCTCTGGTATT	1097
Db	237	ACAGAGGAGGAGGACTTGATGAGTCTCTCTGGAGAAGGGTTGGCTCTGGTATT	296
Qy	1 098	TGGCTGAGGAGGGCCAGGGCCAGGGGGGGGGGGATGGGATGGACCAAGAACATCTCCAC	1157
Db	357	CACCTGAAATCTCCAGAGGACTCTGGTTCTCTGGAGAAGGATACCTCT	416
Qy	1 218	CCTGGGGCAACCTGGGGAGCTTACACACCGGGAGATCTGGCTGGGACCCAG	1277
Db	417	CCTGGGGCAACCTGGGGAGCTTACACACCGGGAGATCTGGCTGGGACCCAG	476
Qy	1 278	TTTCCTCTGAGACACTTACCTCTGCTGGGA 1309	
Db	477	TTTCCTCTGAGACACTTACCTCTGCTGGGA 508	
RESULT 3			
BB246345	BB246345	BB246345	430 bp mRNA linear EST 03-OCT-2001
LOCUS	DEFINITION	TOBAPD2918	Pediatric pre-B cell acute lymphoblastic leukemia
REFERENCE	Authors	Baylor-HGSC project-TCBA	Homo sapiens cDNA clone TOBAP2918, mRNA sequence.
VERSION	VERSION	BB246345	BB246345.1
KEYWORDS	KEYWORDS	EST.	GI:9098094
JOURNAL	JOURNAL	COMMENT	Homo sapiens (human)
ORGANISM	ORGANISM	CONTACT	Dr. Judith P. Margolin
		TEXAS CHILDREN'S CANCER CENTER AND HUMAN GENOME SEQUENCING CENTER	
		AT BAYLOR COLLEGE OF MEDICINE	
		1102 BATTES MC3-3320 HOUSTON, TX 77030, USA	
		TEL: 832-834-4536	
		FAX: 832-835-4038	
		EMAIL: clones@xccc.org	
		CITATION: Carminci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)	
FEATURES	source	Seq primer: M13 primer.	
		Location/Qualifiers	
		1. .430	
		organism="Homo sapiens"	
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		/cell type="pre-B cell"	
		/dev stage="pediatric 2 years"	
		/lab host="DH10B"	
		/clone lib="pediatric pre-B cell acute lymphoblastic	
		leukemia Baylor-HGSC project-TCBA"	
		/notes="Vector: lambda PSB; Site 1: BamHI; Site 2: EcoRI; First strand cDNA was primed with an anchored Xhol-oligo(dT) primer 5'-GAGGATTCGGCCGGCGAGGAGG(T)VN 3'; Primed with a BamHI-dC primer 15'-AGAGAGCTTCCGGCCGATATATATAT(C) 3'.	
		Double-stranded DNA was then digested with BamHI and Xhol and directionally cloned into the BamHI and SalI sites of	

FEATURES
source
High quality sequence stop: 522.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6104649"
/tissue_type="lymphoma, cell line"
/lab_host="DIB10B (phage-resistant)"

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DNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LINC0252 row: k column: 02
High quality sequence stop: 645.

/clone lib=NIH_MGC_95
 /note="Organ: Lymph; Vector: pOTB7; Site 1: XbaI; site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XbaI sites using the following 5' adaptor:
 GGCAGGAG(G). Size-selected >500bp for average insert size
 1.81kb. Library constructed by Ling Hong (University of California, Berkeley)
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."
 BASE COUNT 185 a 223 c 240 g 186 t 2 others
 ORIGIN

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source
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organism="Homo sapiens"
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/clone="IMAGE:5908505"
/tissue_type="lymphoma, cell line"
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ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcorI/XbaI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp or average insert size
1.8kb. Library constructed by Ling Hong in the laboratory"

```

LOCUS B0056204/c
DEFINITION AGECOUNT_6773374 NIH_MGC_99 Homo sapiens cDNA Clone IMAGE:5808505
VERSION 5', mRNA sequence.
ACCESSION B0056204
KEYWORDS B0056204.1 GI:19815544
SOURCE EST.
ORGANISM Homo sapiens (human)
Hom sapiens (human)
Eukaryota; **Metazoa**; **Chordata**; **Craniata**; **Vertebrata**; **Buteleostomi**;
Mammalia; **Euarchonta**; **Primates**; **Catarrhini**; **Hominoidea**; **Homo**.
REFERENCE 1 (bases 1 to 991)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
FAIR USE www.ncbi.nlm.nih.gov

RESULT	6
QY	1034 TCACGAGCTGGCAGACTGTTG 1061
LOCUS	184 TCAGAGCTGGCCAGACTGTTG 157
DEFINITION	AO610898 HS_5103_A2_006_SP6B RPCI-11 Human Male BAC library Homo sapiens genomic clone Plate=681 Col=12 Row=M, genomic survey sequence.
ACCESSION	AO610898
VERSION	AO610898.1
KEYWORDS	GSS
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Qy	245	TGCTATGTTCTGAGTGCTGAGAACAGGACTTACAGACTGAGGAGCC 304	Qy	852	AGAGGAGGAGGAGTGGAGGACACAGAGAGGGCTCACTTCAGGCTACATGAC 911
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Qy	305	TGGGAGGGTTCTCCAGCTCCAGTCCAGTCCAGGAGCTGAGATACCTGGAT 360	Qy	912	CACTCTCTCTGGGGAGAGGAGGAGCTGGGGCTCAGGGCTCGAGGCT?TGGGG 971
Db	303	TGGGAGGGTTCTCCAGCTCCAGTCCAGTCCAGGAGCTGAGATACCTGGAT 358	Db	317	CACTCTCTCTGGGGAGAGGAGGAGCTGGGGCTCAGGGCTCGAGGCT?TGGGG 261
RESULT 8					
LOCUS	BO894374	BO894374_964 bp mRNA linear EST 15-AUG-2002	Qy	972	TGGACTGGGGAGCCAGGCTCTCTGCTCCAAAGCGAGGCTCTGCTGGGATT 1031
DEFINITION	AGENCOURT_8623992 NIH_MGC_99	Homo sapiens cDNA clone IMAGE:6304287	Db	260	CTTCAGAGAGAGCTGGGGCAAGCTCTCTGCTCCAAAGCGAGGCTCTGCTGGGATT 201
VERSION	5'	, mRNA sequence.	Qy	1032	CTTCAGAGAGAGCTGGGGCAAGCTCTCTGCTCCAAAGCGAGGCTCTGCTGGGATT 1061
KEYWORDS	BO894374.1	GI:22286388	Db	200	CTTCAGAGAGAGCTGGGGCAAGCTCTCTGCTCCAAAGCGAGGCTCTGCTGGGATT 171
SOURCE	Homo sapiens (human)				
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 (bases 1 to 964)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished				
COMMENT	Contact: Robert Straussberg, Ph.D. Email: crs@rcm-mail.nih.gov				
RESULT 9					
LOCUS	BY729118	BY729118 PIKEN full-length enriched, 7 days embryo whole body hub	Qy	852	AGAGGAGGAGGAGTGGAGGACACAGAGGGCTCACTTCAGGCTACATGAC 911
DEFINITION	musculus cDNA clone C430033A03	5', mRNA sequence.	Db	377	AAGAGGAGGAGGAGTGGAGGACACAGAGGGCTCACTTCAGGCTACATGAC 318
VERSION	1		Qy	912	CACTCTCTCTGGGGAGAGGAGGAGCTGGGGCTCAGGGCTCGAGGCT?TGGGG 971
KEYWORDS	BY729118.1	GI:27142245	Db	317	CACTCTCTCTGGGGAGAGGAGGAGCTGGGGCTCAGGGCTCGAGGCT?TGGGG 261
SOURCE	Mus musculus (house mouse)				
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 640)				
AUTHORS	Okazaki,Y., Furuno,M., Kanukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaiko,I., Oshio,N., Saito,K., Suzuki,H., Yamamoto,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Goloborod,T., Baldarelli,R., Hill,D.P., Built,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Battalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chitria,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Gariboldi,M., Giassi,C., Forrest,A., Frazer,K.S., Gaasterland,T., Garibaldi,M., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.B., Kanai,A., Kawada,Y., Kederski,R.M., Jackson,I.J., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Magliott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Raven,W.J., Peretea,G., Pesole,G., Petrovsky,N., Pilat,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Rinnwald,M., Sandelin,A., Schneider,C.A., Sepehri,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teadale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,J., Watanabe,Y., Wells,C., Wilming,L.G., Wynnshaw-Boris,A., Yanglisava,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayashita,N., Hizukuri-Kishikawa,T., Kono,H., Nakamura,M., Sakazume,N., Sato,K., Shiraishi,T., Wakai,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,T., Itoh,M., Kaga,A., Miyazaki,I., Sakai,K., Sasaki,D., Shitara,K., Shingawa,A., Yosuishi,A., Yoshino,M., Watanetton,R., Lander,E.S., Rogers,J., Birney,E., and Hayashizaki,Y.				
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	/tissue="lymphoma, cell line"				
	/lab_hosr="DH08 (phage-resistant)"				
	/clone_id="NIH_MGC_99"				
	note="Organ: Lymph-Vector: pCMB7; Site 1: XbaI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into BcRI/XbaI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8 kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and SuperScript II RT (Life Technologies). Note: this is a NIH_MGC Library."				
BASE COUNT	196 a 277 c 268 g 223 t				
ORIGIN					
Query Match	23-74; score 348; DB 13; Length 964;				
Best Local Similarity	98.5%; Pred. No. 62e-69; 1; Indels 5; Gaps 3;				
Matches	384; Conservative 0; Mismatches 1;				
Qy	674	CAGGACTTCTGAGCACACACCTTGAGCAACCTTCAGCCAGGAGTC 732	Qy	733	CGTGTAGTCTCTGAGCACACCTTGAGCAACCTTCAGCCAGGAGTC 498
Db	557	CAGGACTTCTCTGAGCACACCTTGAGCAACCTTCAGCCAGGAGTC 498	Db	733	CGTGTAGTCTCTGAGCACACCTTGAGCAACCTTCAGCCAGGAGTC 791
Qy	733	CGTGTAGTCTCTGAGCACACCTTGAGCAACCTTCAGCCAGGAGTC 791	Db	497	CGTGTAGTCTCTGAGCACACCTTGAGCAACCTTCAGCCAGGAGTC 438
Db	497	CGTGTAGTCTCTGAGCACACCTTGAGCAACCTTCAGCCAGGAGTC 438	Qy	792	CTCGATGTCAGGCCGCGCCACCAAGAACAGAACAGTCAGGAGGAGCTTGAGGAGG 851
Qy	792	CTCGATGTCAGGCCGCGCCACCAAGAACAGAACAGTCAGGAGGAGCTTGAGGAGG 851	Db	437	CTCGATGTCAGGCCGCGCCACCAAGAACAGAACAGTCAGGAGGAGCTTGAGGAGG 378
COMMENT	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 565-573 (2002)				
MEDLINE	2254683				
PUBLISHED	12466831				
CONTACT	Yoshihide Hayashizaki, Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan				
TEL	81-45-503-9222				
FAX	81-45-503-9216				
EMAIL	http://genome.gsc.riken.go.jp/				
	,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda				

QY	487	GCATTCCTGAGGAGCCGGGGAAACAGACCTTTCAGTCAGTCACTCCCATGCCAG	546
Db	564	GAATTCGAGGAGGAGCTCTGGAGACGAGACGACCTCTTCTGACACTCCCTATGCGCAG	623
QY	547	CCAGTCGAGTCACTCT	563
Db	624	CCAGTCGAGTCACTCT	640
		RESULT 10	
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DEFINITION	HS_5_005_A2_D06_SPP6 RPCI-11 Human Male BAC Library	Homo sapiens	GSS 15-JUN-1995
GENOMIC	clone	Plate=681 Col=12 Row=G	genomic survey sequence.
ACCESSION	AQ610868		
VERSION	AQ610868.1	GI:5072144	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens	(human)	
	Bukay-Yoeli, Metzger, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 541)		
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.		
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9733-9744 (1999)		
MEDLINE	99305089		
PUBMED	10449754		
COMMENT			
	Contact: Mahairas GG, Wallace JC, Hood L		
	High Throughput Sequencing Center		
	401 Queen Anne Avenue North, Seattle, WA 98109, USA		
	Tel: (206) 616-3018		
	Fax: (206) 616-3087		
	Email: jwallace@u.washington.edu		
	Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pisterdejong.med.buffalo.edu). Clones may be purchased from BACPC Resources (http://bacpc.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (http://www.ncbi.washington.edu/info/resegen.com). BAC end Web Server: http://www.ncbi.washington.edu		
	Plate: 681 row: G column: 12		
	seq primer: SP6		
	Class: BAC ends		
	High quality sequence stop: 541.		
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	/note=Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;		
	Male blood DNA was isolated from one randomly chosen donor		
	and partially digested with a combination of EcoRI and		
	BcoRI Methylase. Size selected DNA was cloned into the		
	pBAC3.6 vector at BcoRI sites."		
BASE COUNT	100 a 173 c 140 g 125 t	3 others	
ORIGIN			
Query Match	22.8%	Score 335, DB 28, Length 541;	
Best Local Similarity	86.7%	Pred. No. 5, 8e-66;	
Matches	404;	Conservative 0, Mismatches 56, Indels 6, Gaps 3;	
QY	691	CAACACCCCTCTGGACCTTCAGCCAGGAGCCGTCGATGACTTCTCT	750
Db	532	CAACACCCCTCTGGACCTTCAGCCAGGAGCCGTCGATGACTTCTCT	474
QY	751	CTGCTCCCAAGAGGACTGACCGAGGAGGCTCGGCCGACCTCTCGATGGGCGCAG	810

BASE COUNT	113 a	156 c	180 g	109 t
Qy	473 CTGCCCCAAA--GAACTCCAGGAGCTCAAGCCAACTCCCTGAGGCTCCAG 416			
Qy	811 CACCCACAGACAGAATGAGAGGACTTCAAGGAGCAGAGGAGAGATGAGA 870			
Qy	415 CACCAACAGCAGAGATGGAGGAGCTCTGAGAGGAGCTCTGAGAGGAGATGAGA 356			
Qy	871 GGACACAGAGATGCTGCTCACACCTACATTGAACTTCTTCTGGAGCA 930			
Qy	355 GTACACAAAGATGGCTCAAGCTCAAGCTGATTCAGAGGAGACCTTCTGGAGCA 296			
Qy	931 AGAGCACAGAGCTTCAAGGAGCTGAGC??TGTTGGGTGACTCTGGGGCCAG 990			
Qy	295 AGAGCACAGGCTTCAAGGAGCTGAGCAGAC--TGTGGGGGAGACTGGGAGCAG 239			
Qy	991 GGCTCCCTCTGCTCCAGGAGCTGAGGAGATCTCTGGAGAGACTGSC 1050			
Db	238 GGCCTGCTGGGAGGAGAGGGCTCTCTCTCTCTCTCTGGGAGCTGGGACACTGGGACCTTA 60			
Qy	1051 CAGCACTTGACTCTCTGGAGAGCTGAGCTGCTCTGGCTCTGGCTTCTGAGGG 1110			
Qy	178 CAGGGCTTGGACTCTCTCTGAGAGCTGAGGG 119			
Qy	1111 GCGGGGAGAGGGCTGGGATGCGGACCAAGAATCTCTCCCA 1156			
Db	1118 AGCAGGCCAGGGCCGGTGTGATGGCCACAGTCTTCCCCACA 73			
RESULT 11				
LOCUS	AQ634533	558 bp	DNA	linear
DEFINITION	RPCI-11-178C4 TV RPCI-11 Homo sapiens genomic clone RPCI-11-478C4, genomic survey sequence.			
ACCESSION	AQ634533			
VERSION	AQ634533_1			
KEYWORDS	GSS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
RESULT 12				
LOCUS	BI104593	620 bp	mRNA	linear
DEFINITION	EST 26-JUN-2003 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGB:5036481-5, mRNA sequence.			
REFERENCE	BI104593			
AUTHORS	J.C. Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter			
TITLE	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building			
JOURNAL	Unpublished			
COMMENT	Contact: Shaying Zhao, William Nierman, Mark Adams Department of Bukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0200 Email: hb@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.bu.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.bu.edu/order/) or from Research Genet cs (http://info@regen.com). BAC end search page: http://www.tigr.org/tcb/hungen/bac_end_search/bac_end_search.html . seq primer: T7 Class: BAC end.			
FEATURES	source			
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source	/clone="RPCI-11-478C4"			
source	/Sex="Male"			
source	/cell_type="lymphocyte"			
source	/clone_lib="RPCI-11"			
source	/notes="Vector: PRACE3 6; site_1: RCGI; site_2: RCGI;			
RPCI11 Human Male BAC Library				
ORIGIN				
RESULT 13				
LOCUS	BI104593	620 bp	mRNA	linear
DEFINITION	EST 26-JUN-2003 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGB:5036481-5, mRNA sequence.			
REFERENCE	BI104593			
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgbps@remail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.B. Consortium (IIML) DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/IIML at: http://Image.Iml.gov			
FEATURES	source			
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source	/strain="C57BL/10"			
source	/db_xref="GAXON:10090"			
source	/clone="IMAGB:5036481"			
source	/tissue_type="spontaneous tumor, metastatic to mammary"			
source	/stem_cell_origin=""			
source	/lab_host="DHBL"			
source	/clone_lib="NCI_CGAP_Lu29"			
source	/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"			
BASE COUNT	140 a	186 c	168 g	126 t

